

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/845,511

DATE: 06/09/2001
TIME: 06:49:32

CHE 819
819

INPUT SET: S36546.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4 (i)APPLICANT: Thomas, Lawrence J.
5
6 (ii)TITLE OF INVENTION:PLASMID-BASED VACCINE FOR
7 TREATING ATHEROSCLEROSIS
8 (iii)NUMBER OF SEQUENCES: 10
9
10 (iv)CORRESPONDENCE ADDRESS:
11 (A)ADDRESSEE:Yankwich & Associates
12 (B)STREET:130 Bishop Allen Drive
13 (C)CITY:Cambridge
14 (D)STATE:Massachusetts
15 (E)COUNTRY: USA
16 (F)ZIP:02139
17
18 (v)COMPUTER READABLE FORM:
19 (A)MEDIUM TYPE: Floppy disk
20 (B)COMPUTER: IBM PC compatible
21 (C)OPERATING SYSTEM: Windows 95/98
22 (D)SOFTWARE: Word 97
23
24 (vi)CURRENT APPLICATION DATA:
25 (A)APPLICATION NUMBER:(not yet assigned)
26 (B)FILING DATE: 30 April 2001
27 (C)CLASSIFICATION:
28
29 (vii)PRIOR APPLICATION DATA:
30 (A)APPLICATION NUMBER: 08/640,713
31 (B)FILING DATE: 01 May 1996 (01.05.96)
32
33 (vii)PRIOR APPLICATION DATA:
34 (A)APPLICATION NUMBER: 08/302,967
35 (B)FILING DATE: 21 February 1997 (21.02.97)
36
37 (vii)PRIOR APPLICATION DATA:
38 (A)APPLICATION NUMBER: 09/171,969
39 (B)FILING DATE: 29 October 1998 (29.10.98)
40
41 (viii)INVENTOR:
42 (A)NAME:
43 (B)ADDRESS:
44 (C)CITY:
45 (D)STATE:
46 (E)COUNTRY:

EM: 9.10

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/845,511

DATE: 06/09/2
TIME: 06:49:33

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- 47 (2) INFORMATION FOR SEQ ID NO: 1:
- 48 (i) SEQUENCE CHARACTERISTICS:
- 49 (A) LENGTH: 1488 base pairs
- 50 (B) TYPE: nucleic acid
- 51 (C) STRANDEDNESS: single
- 52 (D) TOPOLOGY: linear
- 53 (ii) MOLECULE TYPE: cDNA
- 54 (iii) HYPOTHETICAL:
- 55 (iv) ANTI-SENSE:
- 56 (ix) FEATURE:
- 57 (A) NAME/KEY: Structural coding sequence for
- 58 mature rabbit CETP
- 59 (B) LOCATION:

- 60
- 61 (x) PUBLICATION INFORMATION:
- 62 (A) AUTHORS: Nagashima, Mariko, et al.
- 63 (B) TITLE: Cloning and mRNA tissue
- 64 distribution of rabbit
- 65 cholesteryl ester transfer
- 66 protein
- 67 (C) JOURNAL: J. Lipid Res.
- 68 (D) VOLUME: 29
- 69 (E) ISSUE:
- 70 (F) PAGES: 1642 - 1649
- 71 (G) DATE: 1988
- 72 (K) RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

74 TGTCCECAAAG GCCTCCTCCTA CGAGGCTGGG ATCGTGTGTC GCATCACCAA 50

75

76

77 GCCCGCCCTC TTGGTGTGTA ACCAAGAGAC GGCCAAGGTG GTCCAGACGG 100

78

79 CCTTCCAGCC CGCCGGCTAT CCGGACGTCA GCGGCGAGAG GGCCGTGATG 150

80

81 CTCCTCGGCC GGGTCAAGTA CCGGCTGCAC AACCTCCAGA TCAGCCACCT 200

82

83 GTCGATCGCC AGCAGCCAGG TGGAGCTGGT GGACGCCAAG ACCATCGAGC 250

84

85 TCGCCATCCA GAACGTSTCC GTGGTCTTCA AGGGGACCT GAACTACAGC 300

86

87 TACACGANTG CTTGGGGGTT GGGCATCAAT CAGTCTTTCG ACTTCGAGAT 350

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100
 101 AGGGCCGCCA GCATCCTCTC AGATGGAGAC ATCGGGGTGG ACATTTCCGT 650
 102
 103 GACGGGGGGEC CCTGTCAATCA CAGCCACCTA CCTGGAGTCC CATCACAAAG 700
 104
 105 GTCACCTTCAC GCACAAGAAC GTCTCCGAGG CCTTCCCCCT CCGCGCCTTC 750
 106
 107 CCGCCCCGGTC TTCTGGGGGA CTCCCGCATG CTCTACTTCT GGTTCCTCCGA 800
 108
 109 TCAAGTGCTC AACTCCCTGG CCAGGGCCGC CTCCAGGAG GGCGGTCTCG 850
 110
 111 TGCTCAGCCT GACAGGGGAT GAGTTCAAGA AAGTGCTGGA GACCCAGGGT 900
 112
 113 TTCGACACCA ACCAGGAAAT CTCCAGGAG CTTCCAGAG GCCTTCCCAC 950
 114
 115 CCGCCAGGEC CAGGTAGCCG TCCACTGCCT TAAGGTGCCC AAGATCTCCT1000
 116
 117 GCCAGAACEG GGGTGTCTGT GTGTCTTCTT CCGTCGCCGT GACGTTCCGC1050
 118
 119 TTCCCCCGCC CAGATGGCCG AGAAGCTGTG GCCTACAGGT TTGAGGAGGA1100
 120
 121 TATCATCACC ACCGTCCAGG CCTCCTACTC CCAGAAAAAG CTCTTCCCTAC1150
 122
 123 ACCTCTTBSA TTTCCAGTGC GTGCCGGCCA GCGGAAGGGC AGGCAGCTCA1200
 124
 125 GCAAAATCTET CCGTGGCCCT CAGGAATGAG GCTAAGGCTG TTTCCAAACCT1250
 126
 127 GACTGASASG CGCTCCGAST CCTTCCAGAG CTCTCTCCGC TCCCTGATCG1300
 128
 129 CCACGGTBSG CATCCCBGAG ATCATGTCTC GGCTCGAGGT GGCGTTCCCA1350
 130
 131 GCGCTCATSA ACAGCAAAAG CCTTGGACCTC TTGAAATCA TCAACCCCGSA1400
 132
 133 GATTATCACT CTCGATGGCT GCGTGGTGGT GCAGATGGAC TTCGGTTTTTC1450
 134
 135 CCAAGCACCT GGTGGTGGAT TTCCTCCAGA GCCTGAGC1488

136

137

138

139 (2) INFORMATION FOR SEQ ID NO:2:

140 (i) SEQUENCE CHARACTERISTICS:

141 (A) LENGTH:496 amino acids

142 (B) TYPE:amino acid

143 (C) TOPOLOGY:linear

144 (D) MOLECULE TYPE:protein

145 (E) SYNTHETICAL:NO

146 (F) ANTI-SENSE:NO

147 (G) RECOMBINANT:NO

148 (H) MUTAGENESIS:None

149 (I) ORIGINAL SOURCE:

150 (J) ORGANISM:

151 (K) TISSUE:

152 (L) STRAIN:

153 (M) CELL LINE:

154 (N) CLONING METHOD:

155 (O) REAGENT CATALYST:

156 (P) OTHER:

RAW SEQUENCE LISTING
 PATENT APPLICATION US/09/845,511

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153 (A) AUTHORS:Nagashima, Mariko, et al.
 154 (B) TITLE:Cloning and mRNA tissue
 155 distribution of rabbit
 156 cholesteryl ester transfer
 157 protein
 158 (C) JOURNAL:J. Lipid Res.
 159 (D) VOLUME:29
 160 (E) ISSUE:
 161 (F) PAGES:1643 - 1649
 162 (G) DATE:1988
 163 (H) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 496
 164
 165
 166 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 167
 168 Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys
 169 1 5 10
 170
 171 Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn Gln Glu
 172 15 20 25
 173
 174 Thr Ala Lys Val Val Gln Thr Ala Phe Gln Arg Ala Gly
 175 30 35
 176
 177 Tyr Pro Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu
 178 40 45 50
 179
 180 Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile Ser
 181 55 60 65
 182
 183 His Ieu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp
 184 70 75
 185
 186 Ala Lys Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val
 187 80 85 90
 188
 189 Val Phe Lys Gly Thr Leu Asn Tyr Ser Tyr Thr Ser Ala
 190 95 100
 191
 192 Trp Gly Leu Gly Ile Asn Gln Ser Val Asp Phe Glu Ile
 193 105 110 115
 194
 195 Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu Leu Thr
 196 120 125 130
 197
 198 Val Ala Ala Glu Thr Val Ala Thr Asp Val Thr Tyr Val
 199 135 140 145
 200

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206
 207 Phe Ile Ser Phe Thr Leu Lys Leu Ile Leu Lys Arg Gln
 208 170 175 180
 209
 210 Val Cys Asn Glu Ile Asn Thr Ile Ser Asn Ile Met Ala
 211 185 190 195
 212
 213 Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
 214 200 205
 215
 216 Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro
 217 210 215 220
 218
 219
 220 Val Ile Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly
 221 225 230
 222
 223 His Phe Thr His Lys Asn Val Ser Glu Ala Phe Pro Leu
 224 235 240 245
 225
 226 Arg Ala Phe Pro Pro Gly Leu Leu Gly Asp Ser Arg Met
 227 250 255 260
 228
 229 Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser Leu
 230 265 270
 231
 232 Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser
 233 275 280 285
 234
 235 Leu Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln
 236 290 295
 237
 238 Gly Phe Asp Thr Asn Gln Glu Ile Phe Gln Glu Leu Ser
 239 300 305 310
 240
 241 Arg Gly Leu Pro Thr Gly Gln Ala Gln Val Ala Val His
 242 315 320 325
 243
 244 Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn Arg Gly
 245 330 335
 246
 247 Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe
 248 340 345 350
 249
 250 Phe Arg Ile Asp Gly Ala Glu Met Val Ala Tyr Arg Phe
 251 355 360 365 370 375 380 385 390 395

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/845,511*

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Line	Error	Original Text
25	Wrong application Serial Number	(A)APPLICATION NUMBER:(not yet assigned)